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GOTCAGAGAC	ATCAAGAAAT	AACGCCGGRA	CATTAGTGCA	GGCAGCTTCC	ACAGCAATGG	4200
CATCCTGGTC	ATCCAGCGGA	TAGTTAATGA	TCAGCCCACT	GACCGGTTGC	GCGAGAAGAT	4260
TGTGCACCGC	CGCTTTACAG	GCTTCGACGC	CGCTTCGTTT	TACCATCGAC	ACCACCACGC	4320
TGGCACCCAG	TTGATCGGCG	CGAGATTTAA	TGCGCGCGAC	AATTTCGCGAC	GGCGCGTGCA	4380
GGGCCAGACT	GGAGGTGGCA	ACGCCAATCA	GCAACCACTG	TTTGCCCGCC	AGTTGTTTGT	4440
CCACGCGGTT	GGGAATGTAA	TTGAGCTCCG	CCATCGCCGC	TTCCACTTTT	TCCCGCGTTT	4500
TGCGAGAAAC	GTGGCTGGCC	TGGTTCACCA	CGCGCGAAAC	GGTCTGATAA	GAGACACCGG	4560
CATACTCTGC	GACATCGTAT	AACGTTACTG	GTTTCACATT	CACCAACCTG	AATTGACTCT	4620
CTTCCGGGCG	CTATCATGCC	ATACCCCGAA	AGGTTTTGCG	CCATTCGATG	GTGTCCCGGA	4680
TCTCGACGCT	CTCCCTTATG	CGACTCCTGC	ATTAGGAAGC	AGCCCACTAG	TAGGTTGAGG	4740
CCGTTGAGCA	CCGCCGCCGC	AAGGAATGGT	GCATGCAAGG	AGATGGCGCC	CAACAGTCCC	4800
CCGGCCACGG	GGCCTGCCAC	CATACCCACG	CCGAACAAG	CGCTCTGAG	CCCGAAGTGG	4860
CGAGCCCGAT	CTTCCCCATC	GGTGTGTGCG	GCGATATAGG	CGCCAGCAAC	CGCACCTGTG	4920
GCGCCCGTGA	TGCCCGCCAC	GATGCGTCCG	GCGTAGAGGA	TGGAGATCTC	GATCCCGCGA	4980
AATTAATACG	ACTCACTATA	GGGGAATTGT	GAGCGGATAA	CAATTCCCTT	CTAGAAATAA	5040
TTTTGTTTAA	CTTTAAGAAG	GAGATATACA	TATGGGCCAT	CATCATCATC	ATCACGTGAT	5100
CGACATCATC	GGGACCAGCC	CCACATCCTG	GGAACAGGCG	GCGGCGGAGG	CGGTCCAGCG	5160
GGCGCGGGAT	AGCGTCGATG	ACATCCGCGT	CGCTCGGGTC	ATTGAGCAGG	ACATGGCCGT	5220
GGACAGCGCC	GGCAAGATCA	CTTACCGCAT	CAAQCTCGAA	GTGTGCTTCA	AGATGAGGCC	5280
GGCGCAACCG	AGGGGCTCGA	AACCACCGAG	CGGTTGCGCT	GAAACGGGCG	CCGGCGCGCG	5340
TACTGTGCGG	ACTACCCCGG	CGTCTGCGCC	GGTGACGTTG	GCGGAGACCG	GTAGCACGCT	5400
GCTCTACCCG	CTGTTCAACC	TGTGGCGTCC	GGCCTTTTAC	GAGAGGTATC	CGAAGGTCAC	5460
GATCACCGCT	CAGGGCACCG	GTTCTGGTGC	CGGGATCGCG	CAGGCGCGCG	CCGGGACGCT	5520
CAACATTGGG	GCCTCCGACG	CCTATCTGTC	GGAAGGTGAT	ATGSCCGCGC	ACAAGGGGCT	5580

Fig. 5^D

GATGAACATC	GCGETAGCCA	TCTCGCTCA	GCAGGTCAAC	TACAACTTC	CCGGAGTGAAG	5640
CGAGCACCTC	AAGCTGAACG	GAAAAGTCCT	GGCGGCCATG	TACCAGGCA	CCATCAAAAC	5700
CTGGGACGAC	CCGCAGATCG	CTCGGCTCAA	CCCCGGCGTG	AACCTGCCCC	GCACCGCGGT	5760
AGTTCCGCTG	CACCGCTCCG	ACGGGTCCGG	TCACACCTTC	TTGTTCAACC	AGTACCTGTC	5820
CAAGCAAGAT	CCCGAGGGCT	GGGCAAGTC	GCCCGGCTTC	GSCACCACCG	TCGACTTCCC	5880
GGCGGTGCCG	GTTGCGCTCG	GTGAGAACGG	CAACGGCGGC	ATGTTGACCG	GTTGCGCCGA	5940
GACACCGGCG	TGCTGCGCT	ATATCGGCAT	CAGCTTCCTC	GACCAGGCCA	GTCAAACGGG	6000
ACTCGGCGAG	GCCCAACTAG	GCAATAGCTC	TGGCAATTTT	TTGTTGCCCC	ACGCGCAAAG	6060
CATTCAAGCC	GCGGCGGCTG	GCTTGCATC	GAAAACCCCG	GCGAACCCAGG	CGATTTGGAT	6120
GATCGACGGG	CCCGCCCCGG	ACGGCTACCC	GATCATCAAC	TACGAGTACG	CCATCGTCAA	6180
CAACCGGCAA	AAGGACGCGG	CCACCGGCGA	GACCTTGCGG	GCAATTTCTC	ACTGGGCGAT	6240
CACCGACGGC	AACAAGGCCCT	GTTTCTCGCA	CCAGGTTTCAT	TTCCAGCCCG	TGCGGCGCGG	6300
GCTGGTGAAG	TTGTTCTGAG	GTTTGAATCG	GACGATTTCC	AGCGCTGAGA	TGAAGACCGA	6360
TGCGGCTACC	CTCGCGCGAG	AGGCAGGTAA	TTTCGAGCGG	ATCTCGGCGG	ACCTGAAAC	6420
CCAGATCGAC	CAGGTGGGT	CGACGCGCGG	TTGTTGCGAG	GSCAGTGGC	GCGGCGCGGC	6480
GGGACCGGCG	GCCGAGGCGG	CGTTGGTGGG	CTTCCAAGAA	GCAGCCATA	AGCAGAAGCA	6540
GGAACCTCGAC	GAGATCTCGA	CGAATATTCG	TCAGGCGGGC	GTCCAATACT	CGAGGCGCGA	6600
CGAGGAGCAG	CAGCAGGCGC	TGTTCTCGCA	AATGGGCTTT	GTGCCCCAAA	CGGCGGCTTC	6660
GCGCGGCTCG	ACCGCTGCGG	CGCCACCGCG	ACCGGCGGCA	CCTGTTGCCC	CCCCACCACC	6720
GGCGGCGGCG	AACACGCGGA	ATGCCCCAGCG	GCGCGATCCC	AACGCGGCGC	CTCGGCGGGC	6780
CGACCCGAAC	GCACGCGCGC	CACCTGTTCAT	TGCCCCAAAC	GCACCCCAAC	CTGTCCGGAT	6840
CGACAACCGG	GTTGGAGGAT	TCAGCTTCGC	GCTGCTGCT	GGCTGGGTGG	AGTCTGACGC	6900
CGCCCACTTC	GACTACGGTT	CAGCACTCCT	CAGCAAAAC	ACCGGGGACC	CGCCATTTCC	6960
CGGACAGCGG	CCGCGGTTGG	CCAATGACAC	CGTATCGTG	CTCGGCGGGC	TAGACCRAAA	7020

Fig. 5 E

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GCTTTACGCC	AGGCGCGAAG	CCACCGACTC	CAAGGCCCGG	GCTCGGTTGG	GCTCGGACAT	7080
GGGTGAGTTC	TATATGCCCT	ACCGGGGCAC	CCCGATCAAC	CAGGAAACCG	TCTCGCTTGA	7140
CGCCAAACGG	GTGTCTGGAA	GCGCGTCGTA	TTACGAAGTC	AAGTTCAGCG	ATCCGAGTAA	7200
GCCGAACGGC	CAGATCTGGA	CGGCGGTAAT	CGGCTCGCCC	GCGGCGAAGG	CACCGGACGC	7260
CGGGCCCCCT	CAGCGCTGGT	TTGTGGTATG	GCTCGGGACC	GCCAAACAAC	CGGTGGACAA	7320
GGGCGCGGCC	AAGGCGCTGG	CCGAATCGAT	CCGCGCTTTG	GTGCGCCCGC	CGCCGGCGCC	7380
GGCACCGGCT	CCTGCAGAGC	CCGCTCCGGC	GCTGGCGCGG	GCCGGGGGAG	TGGCTCCTAC	7440
CCCGACGACA	CCGACACCGC	AGCGGACCTT	ACCGGCTTGA	GAATTCTGCA	GATATCCATC	7500
AACTGGCGCG	CCGCTCGAGC	ACCACCACCA	CCACCACTGA	GATCCGGCTG	CTAACAAAGC	7560
CCGAAAGGAA	GCTGAGTTGG	CTGCTGCCAC	CGCTGAGCAA	TAAGTAGCAT	AACCCCTTGG	7620
GGCCTCTAAA	CGGCTCTTGA	GGGGTTTTTT	GCTGAAAGGA	GGAAGTATAT	CCGGAT	7676

Fig. 5F

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Met	Gly	His	His	His	His	His	His	Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser	1	5	10	15
Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala	Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg	20	25	30	
Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	Ala	Arg	Val	Ile	Glu	Gln	Asp	Met	35	40	45	
Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val	50	55	60	
Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	Pro	Arg	Gly	Ser	Lys	Pro	Pro	Ser	65	70	75	80
Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	85	90	95	
Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	100	105	110	
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	115	120	125	
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	130	135	140	
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	145	150	155	160
Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	165	170	175	
Ile	Ser	Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	180	185	190	
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile	195	200	205	
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn	210	215	220	

Fig. 5G

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Leu	Pro	Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly		
225					230					235					240		
Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly		
			245						250					255			
Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val		
			260					265						270			
Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys		
		275					280					285					
Ala	Glu	Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp		
	290					295						300					
Gln	Ala	Ser	Gln	Arg	Gly	Leu	Gly	Glu	Ala	Gln	Leu	Gly	Asn	Ser	Ser		
305					310						315				320		
Gly	Asn	Phe	Leu	Leu	Pro	Asp	Ala	Gln	Ser	Ile	Gln	Ala	Ala	Ala	Ala		
			325						330					335			
Gly	Phe	Ala	Ser	Lys	Thr	Pro	Ala	Asn	Gln	Ala	Ile	Ser	Met	Ile	Asp		
			340					345						350			
Gly	Pro	Ala	Pro	Asp	Gly	Tyr	Pro	Ile	Ile	Asn	Tyr	Glu	Tyr	Ala	Ile		
	355						360					365					
Val	Asn	Asn	Arg	Gln	Lys	Asp	Ala	Ala	Thr	Ala	Gln	Thr	Leu	Gln	Ala		
	370					375					380						
Phe	Leu	His	Trp	Ala	Ile	Thr	Asp	Gly	Asn	Lys	Ala	Ser	Phe	Leu	Asp		
385				390						395				400			
Gln	Val	His	Phe	Gln	Pro	Leu	Pro	Pro	Ala	Val	Val	Lys	Leu	Ser	Asp		
			405						410					415			
Ala	Leu	Ile	Ala	Thr	Ile	Ser	Ser	Ala	Glu	Met	Lys	Thr	Asp	Ala	Ala		
		420						425					430				
Thr	Leu	Ala	Gln	Glu	Ala	Gly	Asn	Phe	Glu	Arg	Ile	Ser	Gly	Asp	Leu		
	435						440						445				
Lys	Thr	Gln	Ile	Asp	Gln	Val	Glu	Ser	Thr	Ala	Gly	Ser	Leu	Gln	Gly		
	450					455					460						
Gln	Trp	Arg	Gly	Ala	Ala	Gly	Thr	Ala	Ala	Gln	Ala	Ala	Val	Val	Arg		
465					470					475					480		

Fig. 5 H

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Phe	Gln	Glu	Ala	Ala	Asn	Lys	Gln	Lys	Gln	Glu	Leu	Asp	Glu	Ile	Ser	485	490	495	
Thr	Asn	Ile	Arg	Gln	Ala	Gly	Val	Gln	Tyr	Ser	Arg	Ala	Asp	Glu	Glu	500	505	510	
Gln	Gln	Gln	Ala	Leu	Ser	Ser	Gln	Met	Gly	Phe	Val	Pro	Thr	Thr	Ala	515	520	525	
Ala	Ser	Pro	Pro	Ser	Thr	Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	530	535	540	
Val	Ala	Pro	Pro	Pro	Pro	Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	545	550	555	560
Gly	Asp	Pro	Asn	Ala	Ala	Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	565	570	575	
Pro	Pro	Val	Ile	Ala	Pro	Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn	580	585	590	
Pro	Val	Gly	Gly	Phe	Ser	Phe	Ala	Leu	Pro	Ala	Gly	Trp	Val	Glu	Ser	595	600	605	
Asp	Ala	Ala	His	Phe	Asp	Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr	610	615	620	
Gly	Asp	Pro	Pro	Phe	Pro	Gly	Gln	Pro	Pro	Pro	Val	Ala	Asn	Asp	Thr	625	630	635	640
Arg	Ile	Val	Leu	Gly	Arg	Leu	Asp	Gln	Lys	Leu	Tyr	Ala	Ser	Ala	Glu	645	650	655	
Ala	Thr	Asp	Ser	Lys	Ala	Ala	Ala	Arg	Leu	Gly	Ser	Asp	Met	Gly	Glu	660	665	670	
Phe	Tyr	Met	Pro	Tyr	Pro	Gly	Thr	Arg	Ile	Asn	Gln	Glu	Thr	Val	Ser	675	680	685	
Leu	Asp	Ala	Asn	Gly	Val	Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	690	695	700	
Phe	Ser	Asp	Pro	Ser	Lys	Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	705	710	715	720
Gly	Ser	Pro	Ala	Ala	Asn	Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	725	730	735	

Fig. 5 I

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Phe	Val	Val	Trp	Leu	Gly	Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala
			740					745					750		
Ala	Lys	Ala	Leu	Ala	Glu	Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro
		755					760					765			
Ala	Pro	Ala	Pro	Ala	Pro	Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala
	770					775					780				
Gly	Glu	Val	Ala	Pro	Thr	Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu
785					790					795					800
Pro	Ala														

Fig. 5J

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Fig. 73

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[illegible]

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Fig. 9A

CAAAACCCGAAAGGAAAGCTGA
GTTTCGGGCTTTCCTTCACT
G S P K G S

Fig. 9B

10

[illegible]

1894
 1895
 1896

GTGATCTACGAGCAGGCCAACGCCACGGGCAAGAGGTGACGGCTGCGGCAACAACTGGGCAAAACGACAGCGCGTCCGGTCCAGCTGGGCACTA
 CACTAGATGCTCGTCCGGTTGGGGGTGCCCGTCTTCCAGGTCCGAGGGCGGTCTTTGTACCGCGTTTGGCTGTCCGGGACGCCAGGTGAGTCCCGTAT 100
 Y I Y E Q A N A N G S K Y Q A A G N N H A S T D S A V G S S W A T
 GTAACGCCGCCAGTGTGCTGGAATTCTGAGATATCCATCACTGGCGGCCGCTGAGGACAGATCCGGTCTGTAACAAAGCCGAAAGGAAGTGAATT 110
 CATTCGCCGGGGTCAACAGACCTTAAGACGTCTATAGGTAGTGTGACCCGCCGAGCTGCTCTAGGCGACGATTGTTTCGGGCTTTCTCTGACTCA
 S N G R G C A G I L D I S I T L A A A R A D P A A N K A R K E A E L
 GGCT
 --- 1104
 CCBA
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Fig. 13

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[illegible]

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Fig. 12A

GGGTTTGGGACCTGGCCGTGTGGAGGCGAGAAATACCCGACCGCTGTGTTGGGACGAGTGGTSCAAAGCTGTGTACCGCCGACAGTTTAT
 CCGAAAACGCTGAGCGGACACGCTGCCGCTTTCATGGGGCTGGGAGCAAAACCTGGCTACCTACCTTTGCACCAATGCGCCGGTGTCAAAATG 800

G F G D L A V C G G E X Y P D G S F W H G W M G Y W F Y G P G F Y
 G Y L A T M P C A T A R S T P T A R F G T S G C R R G L P A H S F T
 G F W R L G R Y R R R E V P R R L V L A P V D A N Y V Y R P T Y L

Dra III
Pvu II
Xba I
EcoRI
 TTGGATTGTGTGACGGGGGTGAGCCCTCCCGGCGCGGCGCCACCGGCTGTGCGGTGGGCAATTCCTGCGAGCAGCCCAAGCTCCCTGAGAAAT 700
 AAGCTACACAGTCCCGGCACTCGGGAGCGGCGCGCGGCGGCTGGCCCAAGCGCCACCGCTTACGCCAGGCTCGTGGGTTCGAGGAGACTCTTA

F D C Y S G G E F L F G P P P P G G C G G A I P S E O P H A P . E
 S I Y S A A Y S P S P A R R H R Y V A Y G G F R P S S P T L P E N
 L R L C G R . A P P R P A A T G W L R W G N S Y R A A G R S L R

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Fig. 13B

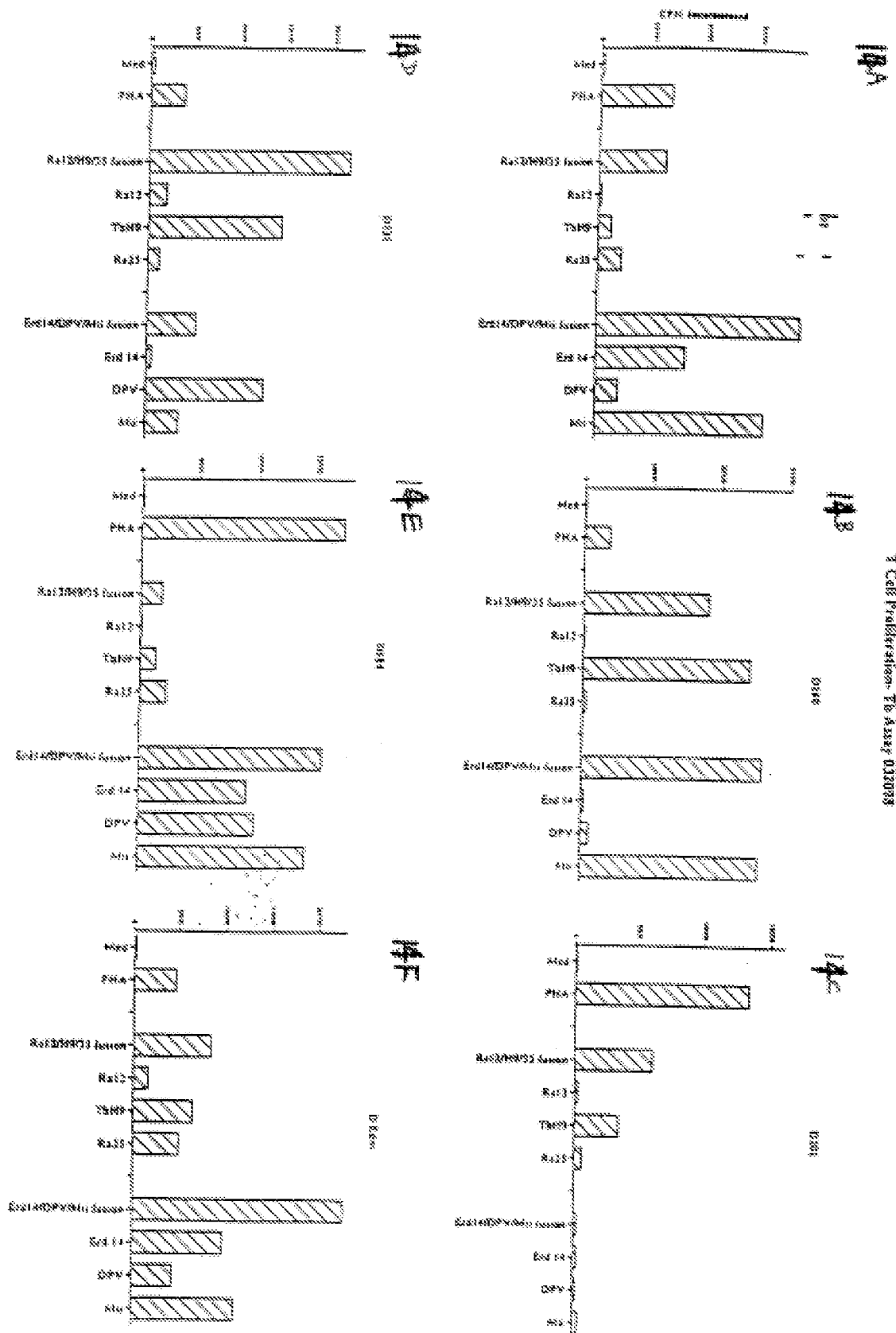
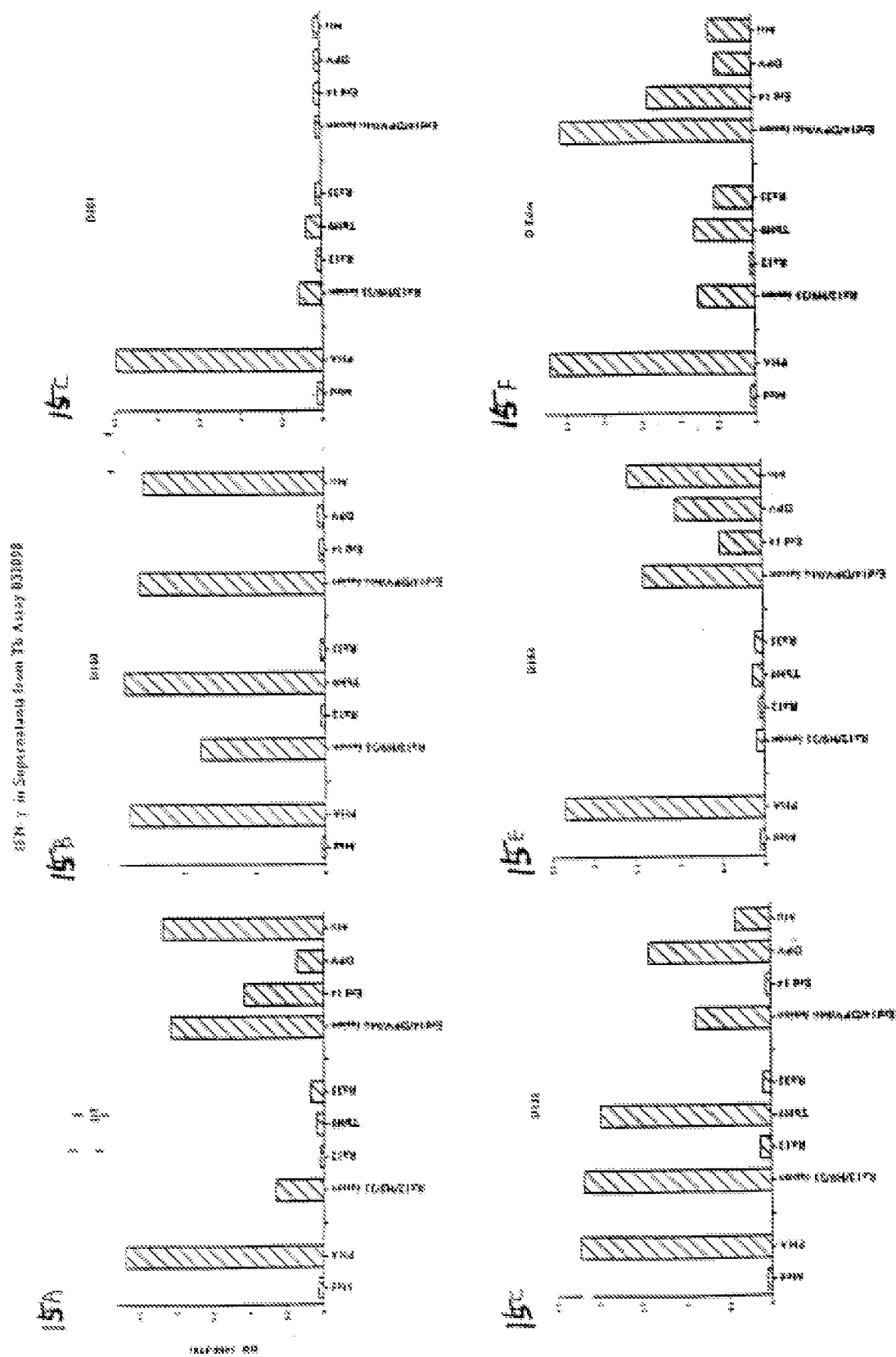
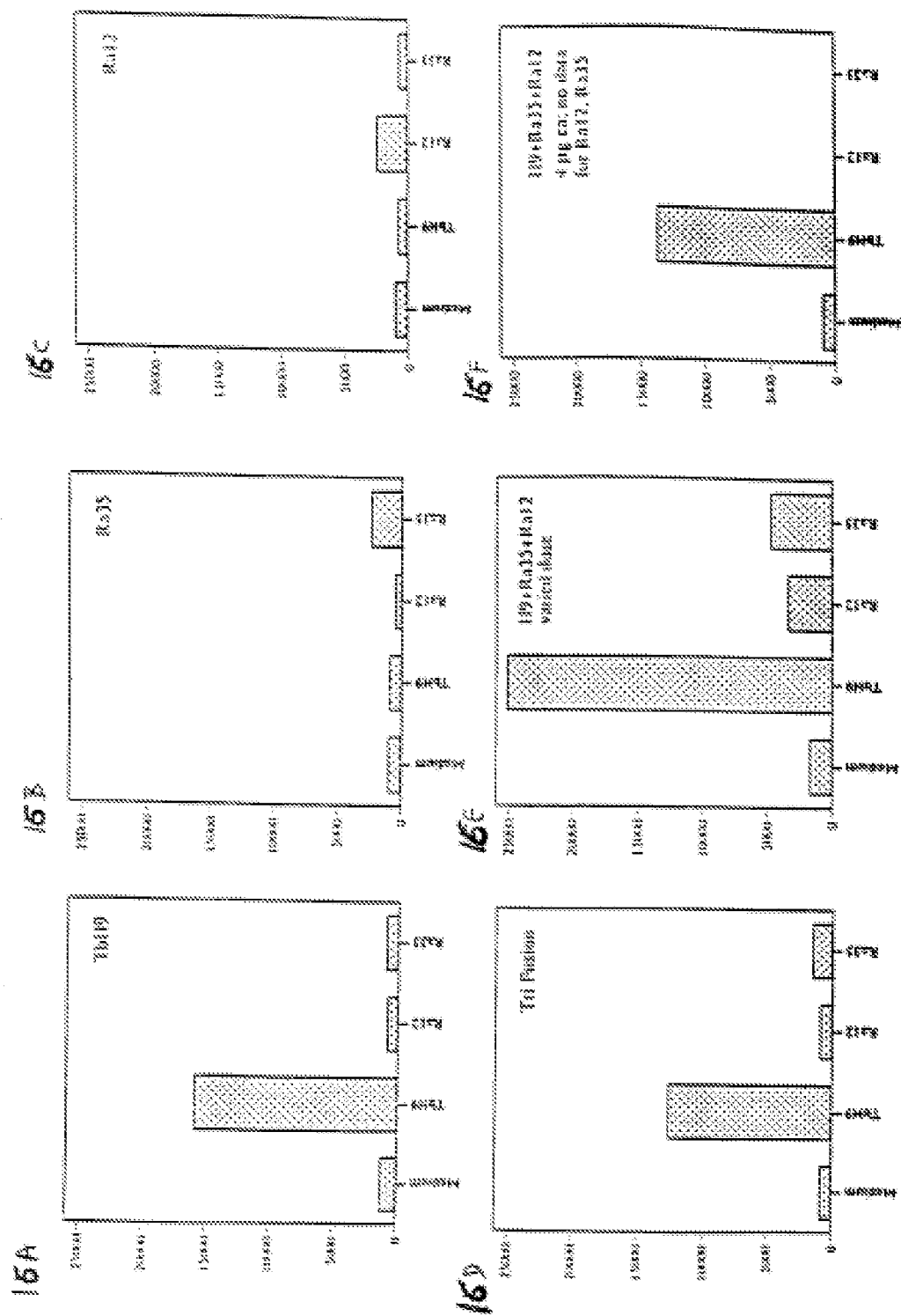


Fig. 14A-14F



Syllabus



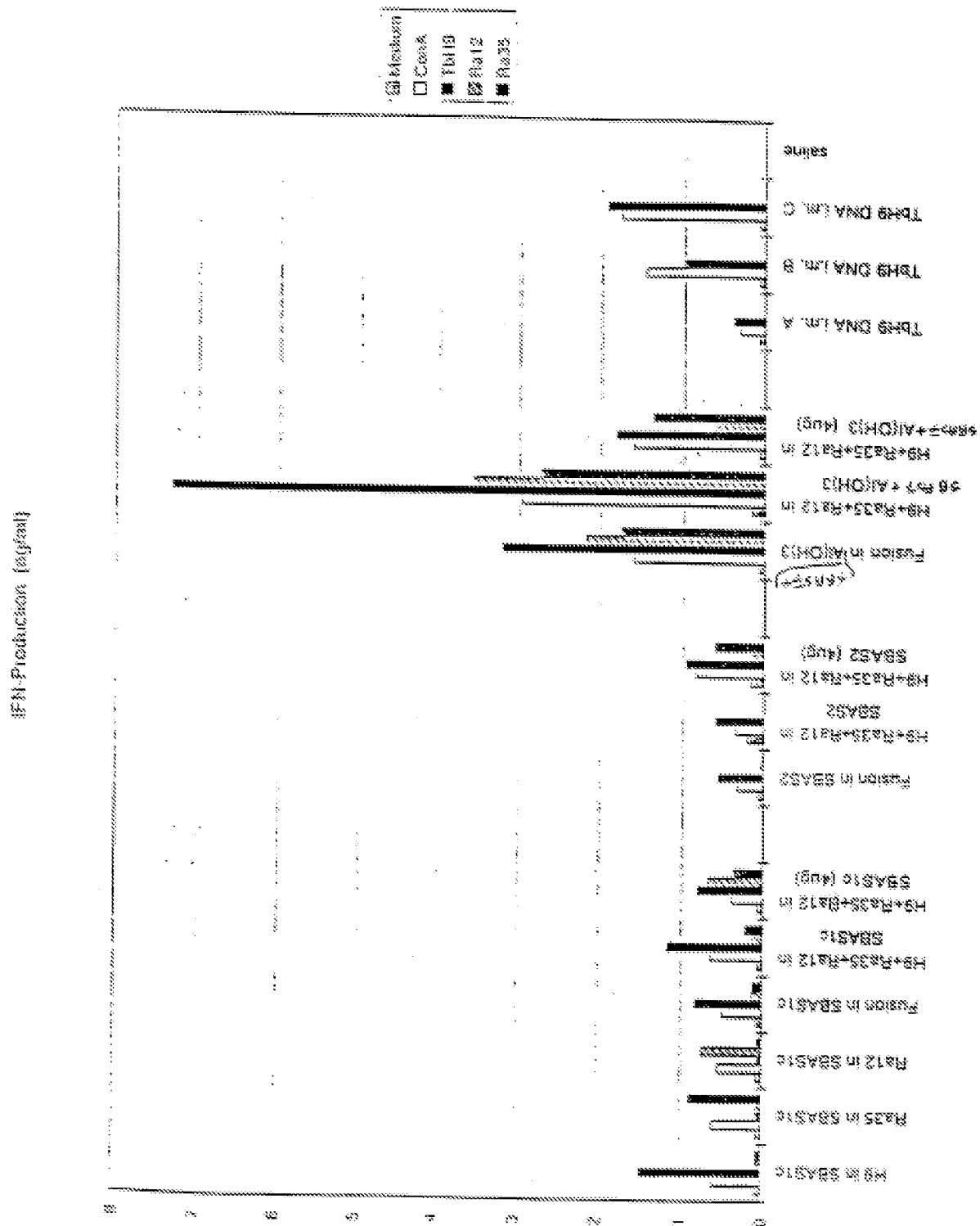


Fig. 7

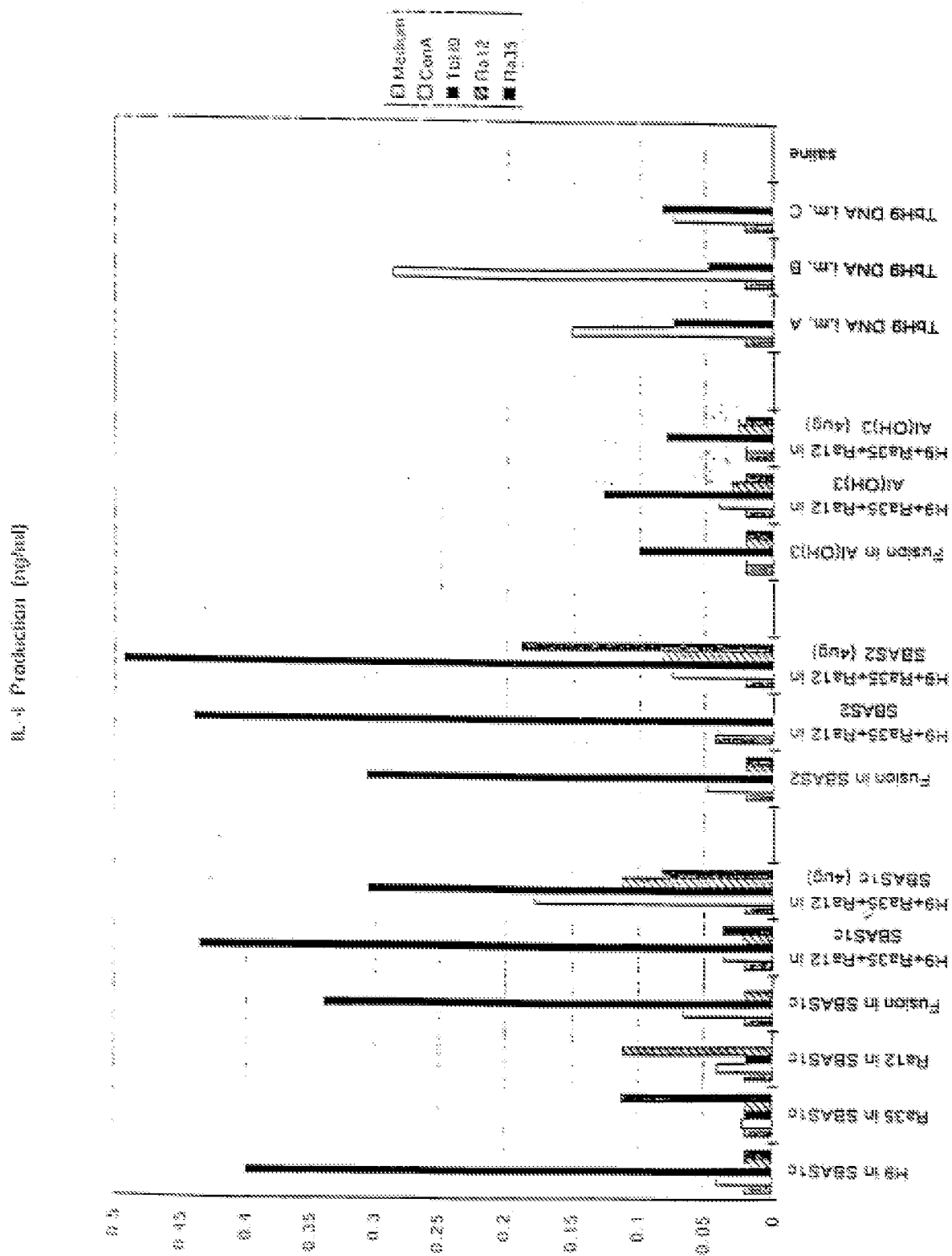


Fig. 18

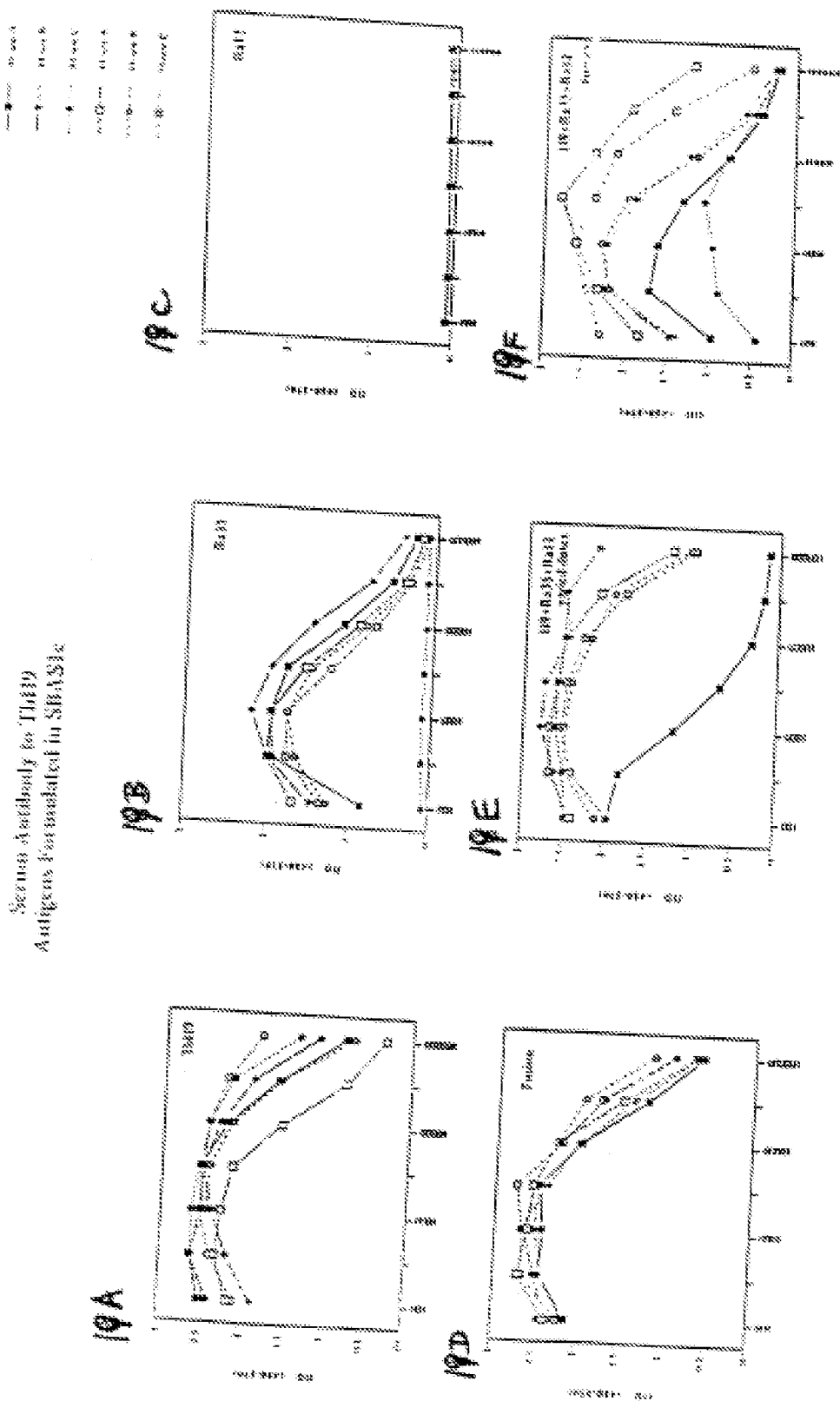
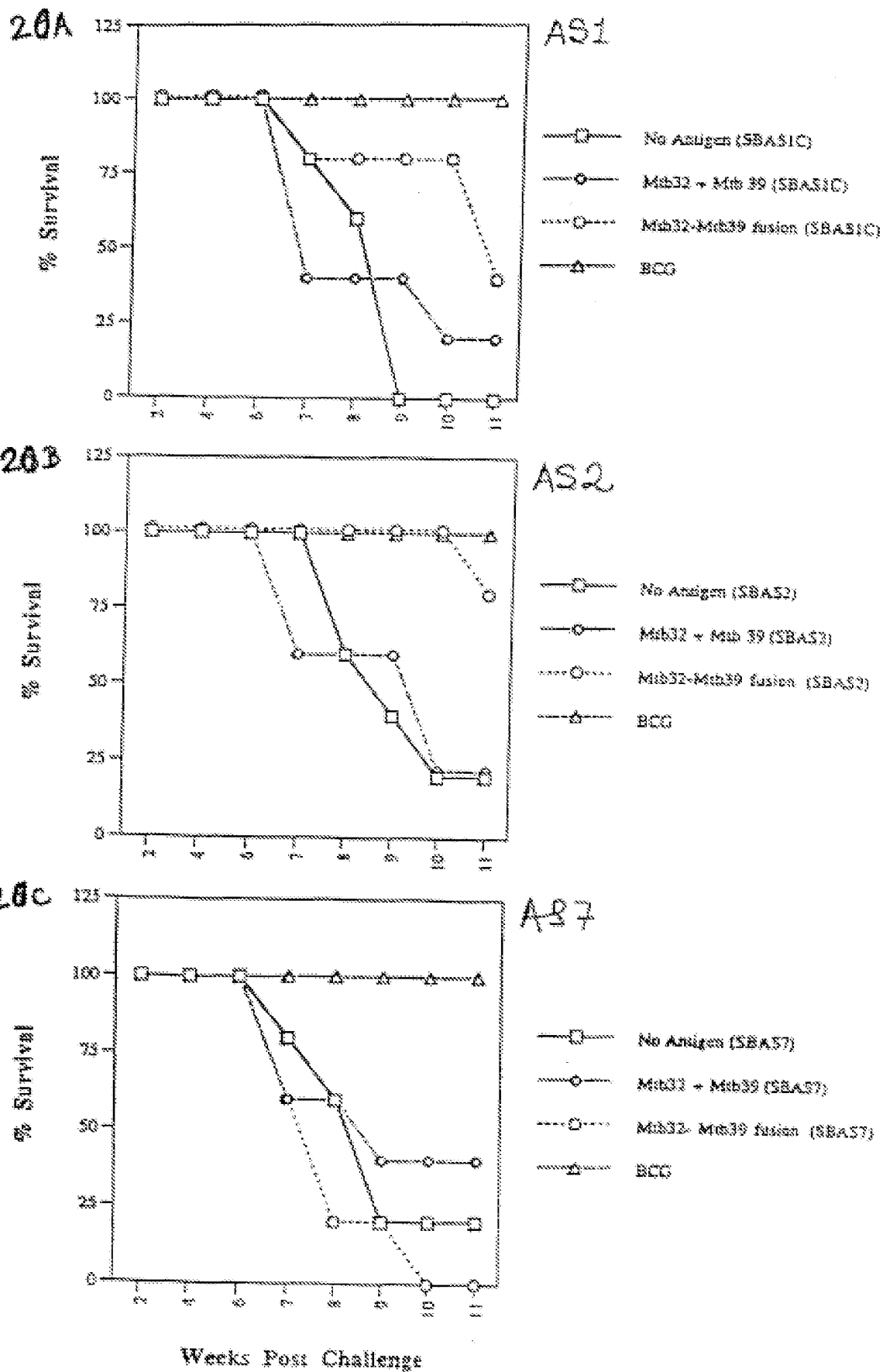
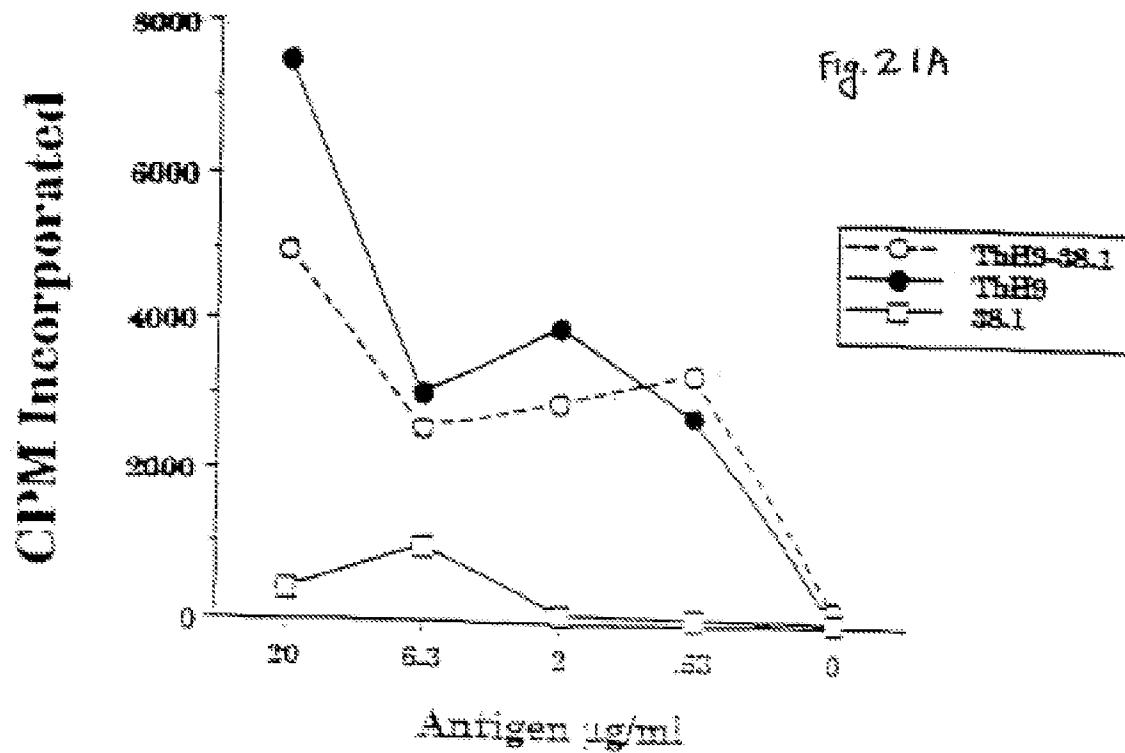


Fig 19A-19F

Fig. 20A-20C



D131 T Cell Proliferation



D131 IFN γ

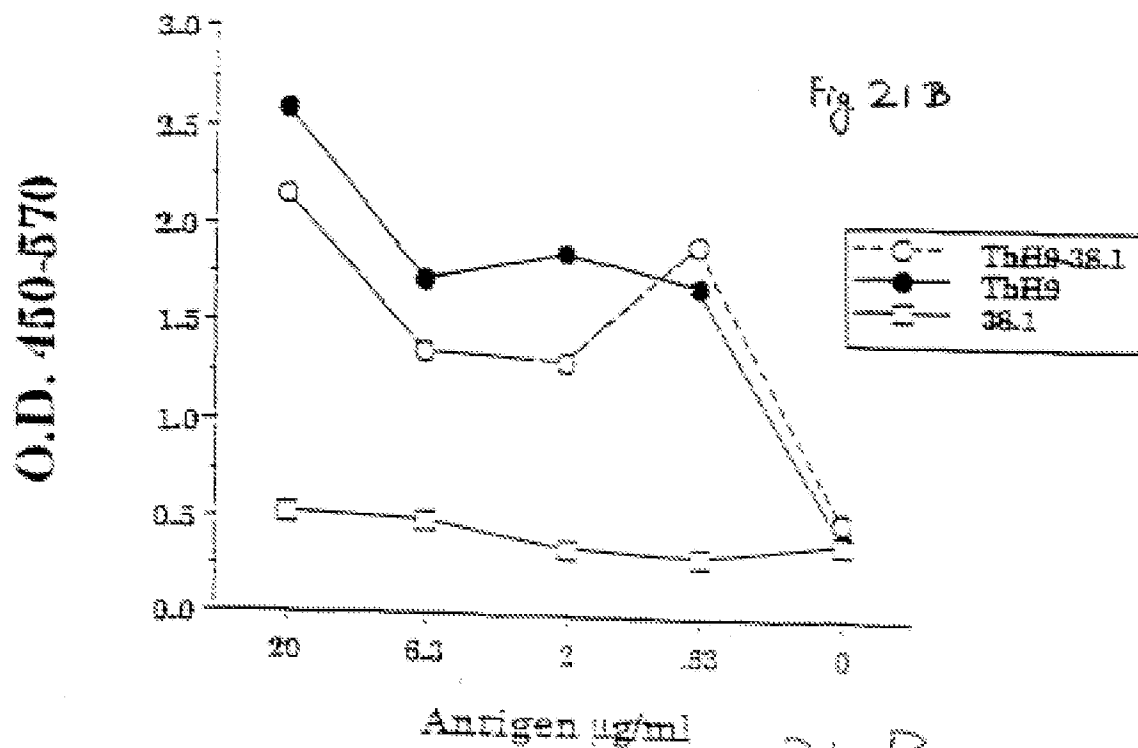
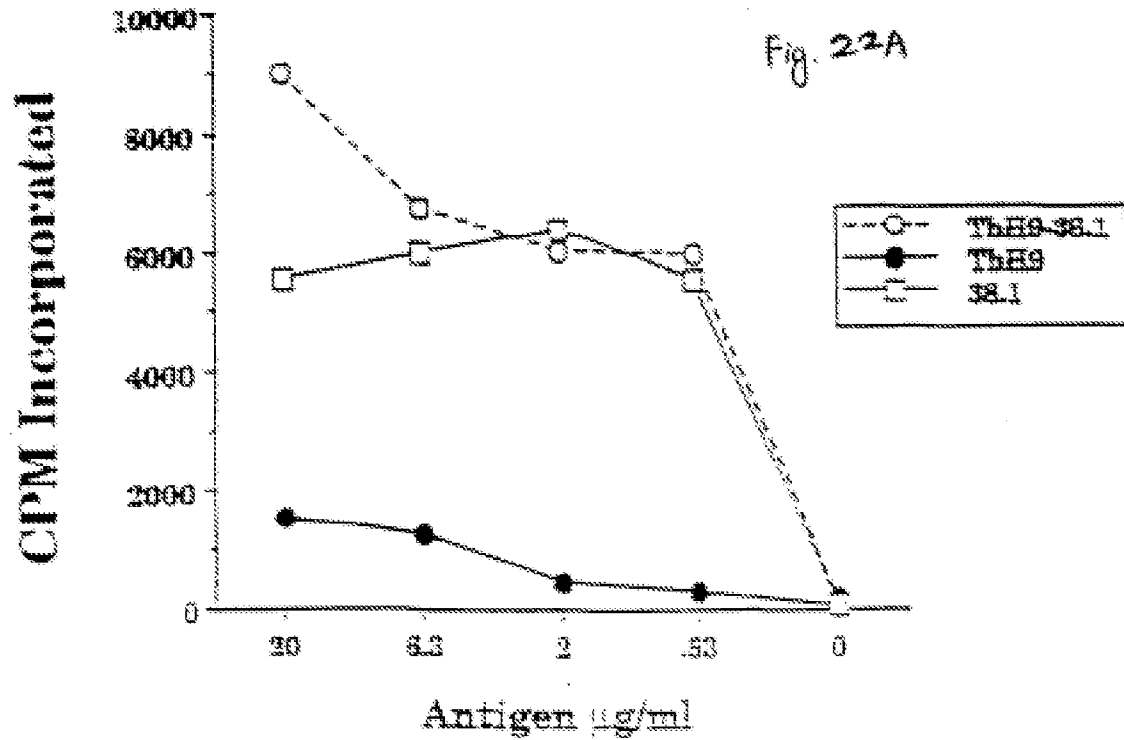


Fig. 21A + 21B

D184 T Cell Proliferation



D184 IFN γ

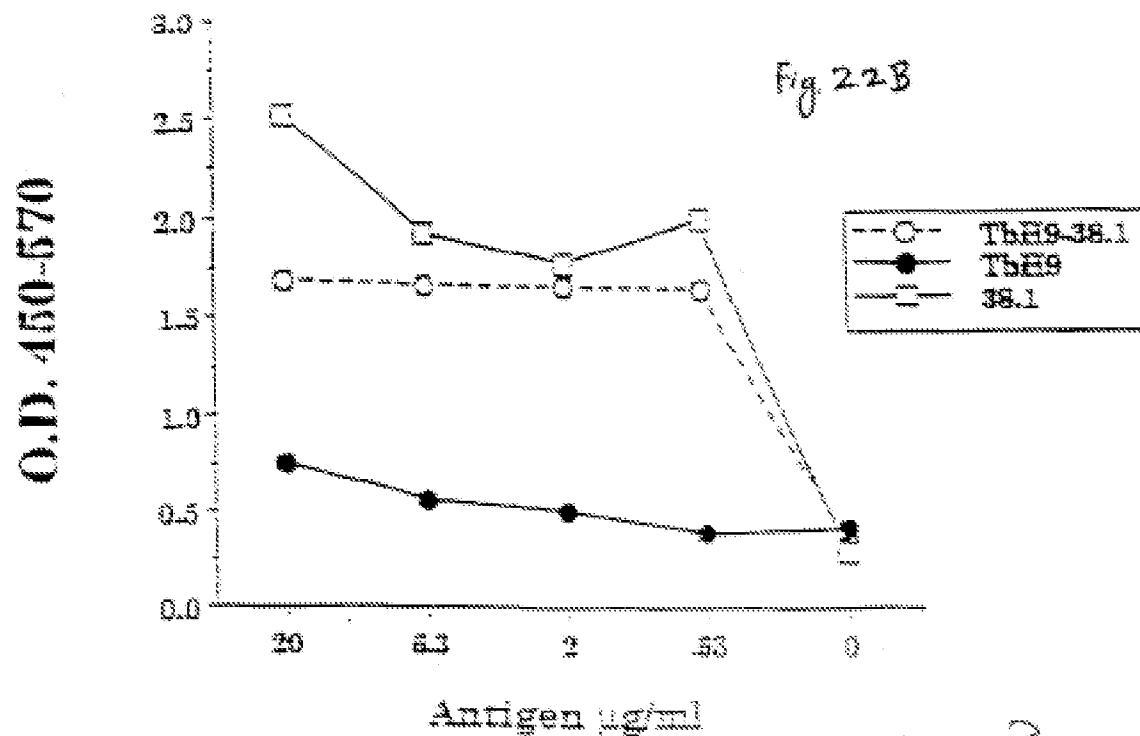


Fig. 22A + 22B

Fig. 23A

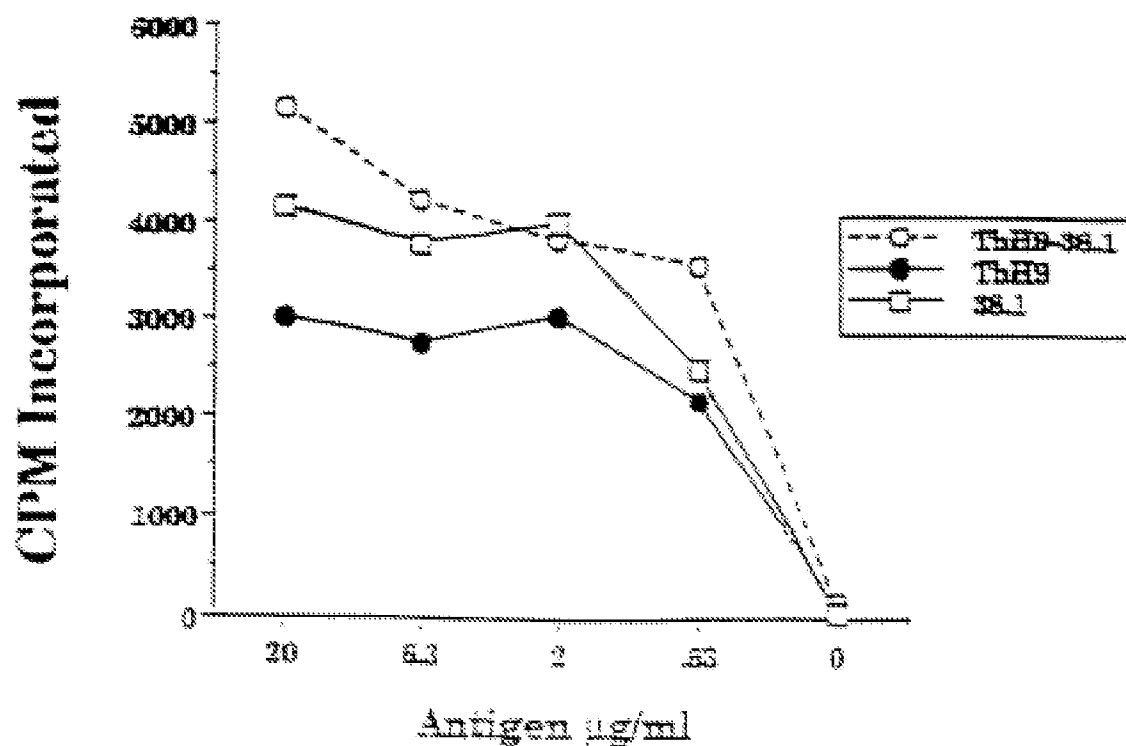
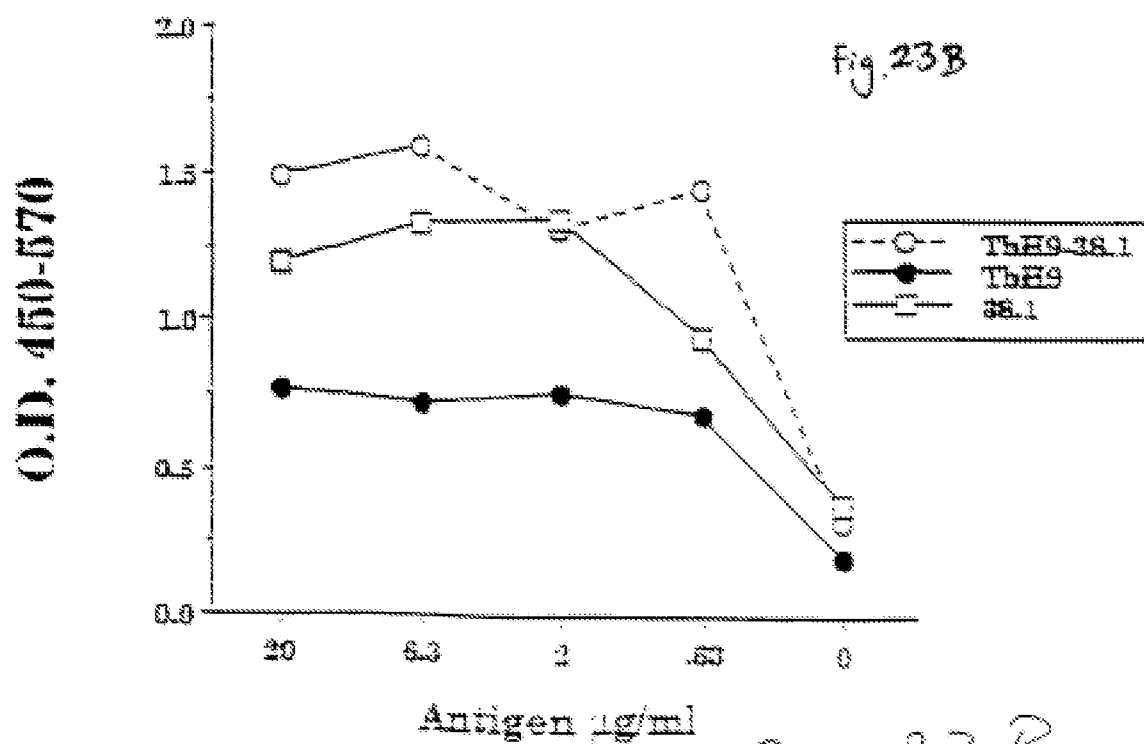
D201 T Cell Proliferation**D201 IFN γ** 

Fig. 23B

Fig. 23 A + 23B